Figure 1
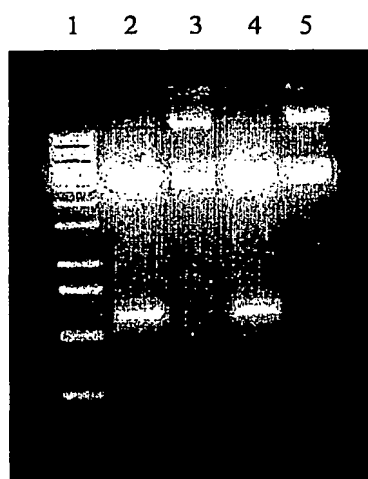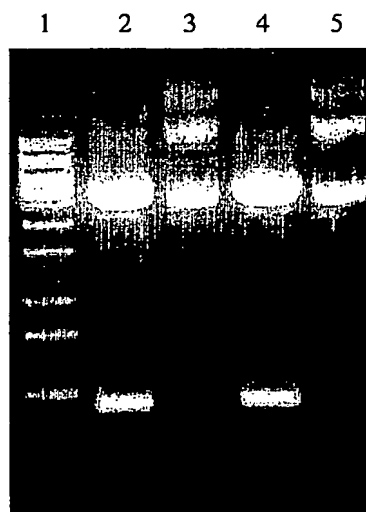

Figure 2

Figure 3A

```
Query:  40  EGRAAELARKLEATASAKNLVEQDXXXXXXXXXXXXXXXIAEVRAAELAGVLEATAAAKTAV  99
            E RAAELA +LEATA+AK+  EQD                +E RAAELA  LEATAAAK +
Sbjct: 712  EERAAELASQLEATAAAKSSAEQDRENTRATLEQQLRESEARAAELASQLEATAAAKMSA  771


Query: 100  EQERERTRAALXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXKTSVEQXXXXXXXXXXXXXXXXXXXXXX  159
            EQ+RE TRA L                             K S EQ
Sbjct: 772  EQDRENTRATLEQQLRDSEERAAELASQLESTTAAKMSAEQDRESTRATLEQQLRDSEER  831


Query: 160  XXXXXXXXXKSTAAVKSAMEQDRENTRAT 187
            +ST A K +  EQDRE+TRAT
Sbjct: 832  AAELASQLESTTAAKMSAEQDRESTRAT 859
```

Figure 3B

```
Query:  29  EQEREKTRTALE-------GRAAELARKLEATASAKNLVEQDXXXXXXXXXXXXXXXIAEVR  81
            EQ+RE TR  LE          RAAELA +LEATA+AK  EQD            +E R
Sbjct: 733  EQDRENTRATLEQQLRESEARAAELASQLEATAAAKMSAEQDRENTRATLEQQLRDSEER  792


Query:  82  AAELAGVLEATAAAKTAVEQERERTRAALXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXKTSVEQX  141
            AAELA  LE+T AAK +  EQ+RE TRA L                             K S EQ
Sbjct: 793  AAELASQLESTTAAKMSAEQDRESTRATLEQQLRDSEERAAELASQLESTTAAKMSAEQD  852


Query: 142  XXXXXXXXXXXXXXXXXXXXXXXXXXXXXKSTAAVKSAMEQDRENTRAT 187
            +ST A K +  EQDRE+TRAT
Sbjct: 853  RESTRATLEQQLRESEERAAELASQLESTTAAKMSAEQDRESTRAT 898
```

Figure 3C

```
Query:  29  EQEREKTRTALEG-------RAAELARKLEATASAKNLVEQDXXXXXXXXXXXXXIAEVR  81
            EQ+RE TR  LE       RAAELA +LE+T +AK   EQD            +E R
Sbjct: 772  EQDRENTRATLEQQLRDSEERAAELASQLESTTAAKMSAEQDRESTRATLEQQLRDSEER  831


Query:  82  AAELAGVLEATAAAKTAVEQERERTRAALXXXXXXXXXXXXXXXXXXXXXXXXXXXKTSVEQX  141
            AAELA  LE+T AAK + EQ+RE TRA L                          K S EQ
Sbjct: 832  AAELASQLESTTAAKMSAEQDRESTRATLEQQLRESEERAAELASQLESTTAAKMSAEQD  891


Query: 142  XXXXXXXXXXXXXXXXXXXXXXXXXXXXKSTAAVKSAMEQDRENTRA  186
                                        ++TAA KS+ EQDRENTRA
Sbjct: 892  RESTRATLEQQLRDSEERAAELASQLEATAAAKSSAEQDRENTRA  936
```

Figure 3D

```
Query:  40  EGRAAELARKLEATASAKNLVEQDXXXXXXXXXXXXXXIAEVRAAELAGVLEATAAAKTAV  99
            E RAAELA +LEATA+AK+  EQD          +E RAAELA  LEATAAAK +
Sbjct: 712  EERAAELASQLEATAAAKSSAEQDRENTRATLEQQLRESEARAAELASQLEATAAAKMSA  771


Query: 100  EQERERTRAALXXXXXXXXXXXXXXXXXXXXXXXXXXXXXKTSVEQXXXXXXXXXXXXXXXXXXXXXXX  159
            EQ+RE TRA L                          K S EQ
Sbjct: 772  EQDRENTRATLEQQLRDSEERAAELASQLESTTAAKMSAEQDRESTRATLEQQLRDSEER  831


Query: 160  XXXXXXXXKSTAAVKSAMEQDRENTRAT  187
                    +ST A K + EQDRE+TRAT
Sbjct: 832  AAELASQLESTTAAKMSAEQDRESTRAT  859
```

Figure 3E

```
Query:  29  EQEREKTRTALE-------GRAAELARKLEATASAKNLVEQDXXXXXXXXXXXXXXIAEVR  81
            EQ+RE TR  LE        RAAELA +LEATA+AK    EQD                +E R
Sbjct: 733  EQDRENTRATLEQQLRESEARAAELASQLEATAAAKMSAEQDRENTRATLEQQLRDSEER  792


Query:  82  AAELAGVLEATAAAKTAVEQERERTRAALXXXXXXXXXXXXXXXXXXXXXXXXXXXXKTSVEQX  141
            AAELA  LE+T AAK +  EQ+RE TRA L                            K S EQ
Sbjct: 793  AAELASQLESTTAAKMSAEQDRESTRATLEQQLRDSEERAAELASQLESTTAAKMSAEQD  852


Query: 142  XXXXXXXXXXXXXXXXXXXXXXXXXXXXKSTAAVKSAMEQDRENTRAT  187
                                        +ST A K +  EQDRE+TRAT
Sbjct: 853  RESTRATLEQQLRESEERAAELASQLESTTAAKMSAEQDRESTRAT  898
```

Figure 3F

```
Query:  29  EQEREKTRTALEG-------RAAELARKLEATASAKNLVEQDXXXXXXXXXXXXXXIAEVR  81
            EQ+RE TR  LE        RAAELA +LE+T +AK    EQD        .       +E R
Sbjct: 772  EQDRENTRATLEQQLRDSEERAAELASQLESTTAAKMSAEQDRESTRATLEQQLRDSEER  831 .


Query:  82  AAELAGVLEATAAAKTAVEQERERTRAALXXXXXXXXXXXXXXXXXXXXXXXXXXXXXKTSVEQX  141
            AAELA  LE+T AAK +  EQ+RE TRA L                            K S EQ
Sbjct: 832  AAELASQLESTTAAKMSAEQDRESTRATLEQQLRESEERAAELASQLESTTAAKMSAEQD  891


Query: 142  XXXXXXXXXXXXXXXXXXXXXXXXXXXXKSTAAVKSAMEQDRENTRA  186
                                        ++TAA KS+  EQDRENTRA
Sbjct: 892  RESTRATLEQQLRDSEERAAELASQLEATAAAKSSAEQDRENTRA  936
```

Figure 4

```
LCIMM   121 GAGCAGCAGCTTCGCGAATCCGAGGCGCGCGCTGCGGAGCTGGCGAGCCAGCTGGAGGCC 180
KEIMM     1 ------------------------------------------------------------   1
DDIMM     1 GAGCAGCAGCTTCGTGAATCCGAGGCGCGCGCTGCGGAGCTGAAAGCCGAGCTGGAGGCC  60

LCIMM   181 ACTGCTGCTGCGAAGATGTCAGCGGAGCAGGACCGCGAGAACACGAGGGCCACGCTAGAG 240
KEIMM     1 --------------------------------------------------------GAG   3
DDIMM    61 ACTGCTGCTGCGAAGACGTCGGTGGAGCAGGAGCGTGAGAAGAC------------GAG 107

LCIMM   241 CAGCAGCTTCGTGACTCCGAGGAGCGCGCTGCGGAGCTGGCGAGCCAGCTGGAGTCCACT 300
KEIMM     4 CAGCAGCTTCGTGACTCCGAGGAGCGCGCTGCGGAGCTGATGCGGAAGTTAGAGGCGACT  63
DDIMM   108 GA-CGGCTCTG------GAGGGGCGCGCTGCGGAGCTGGCTCGCAAACTGGAGGCGACT 159

LCIMM   301 ACTGCTGCGAAGATGTCAGCGGAGCAGGACCGCGAGAGCACGAGGGCCACGCTAGAGCAG 360
KEIMM    64 GCTGCTGCGAAGTCGTCGGCGGAGCAGGACCGCGAGAACACGAGGGCCACGTTGGAGCAG 123
DDIMM   160 GCTTCTGCGAAGAATTTGGTAGAGCAGGACCGCGAGAGGACGAGGGCCACCTTGGAGGAA 219

LCIMM   361 CAGCTTCGTGACTCCGAGGAGCGCGCTGCGGAGCTGGCGAGCCAGCTGGAGTCCACTACT 420
KEIMM   124 CAGCTTCGCGAATCCGAGGAGCACGCTGCGGAGCTGAAGGCCCAGCTGGAGTCCACTGCT 183
DDIMM   220 CGACTTCGTATTGCTGAGGTGCGCGCTGCGGAGCTGGCAGGAGTGCTGGAGGCCACTGCT 279

LCIMM   421 GCTGCGAAGATGTCAGCGGAGCAGGACCGCGAGAGCACGAGGGCCACGCTAGAGCAGCAG 480
KEIMM   184 GCTGCGAAGACGTCGGCGGAGCAGGACCGCGAGAACACGAGGGCCGCGTTGGAGCAGCGG 243
DDIMM   280 GCTGCGAAGACGGCGGTGGAGCAGGAGCGTGAGAGGACGAGGGCCGCCTTGGAGCAGCAG 339

LCIMM   481 CTTCGCGAATCCGAGGAGCGCGCTGCGGAGCTGGCGAGCCAGCTGGAGTCCACTACTGCT 540
KEIMM   244 CTTCGCGAATCCGAGGAGCGCGCTGCGGAGCTGGCGAGCCAGCTGGAGGCCACTGCTGCT 303
DDIMM   340 CTCCGCGAATCCGAGGCGCGCGCTGCGGAGCTGGCTGCGCAGCTGGAAGCCGCTGCTGCG 399

LCIMM   541 GCGAAGATGTCAGCGGAGCAGGACCGCGAGAGCACGAGGGCCACGCTAGAGCAGCAGCTT 600
KEIMM   304 GCGAAGTCGTCGGCGGAGCAGGACCGCGAGAACACGAGGGCCACGCTAGAGCAGCAGCTT 363
DDIMM   400 GCGAAGACGTCGGTGGAGCAGGAGCGTGAGAACACGAGGGCCACCTTGGAGCAGCGGTTG 459

LCIMM   601 CGTGACTCCGAGGAGCGCGCTGCGGAGCTGGCGAGCCAGCTGGAGGCCACTGCTGCTGCG 660
KEIMM   364 CGCGAATCCGAGCCGCGCGCTGCGGAGCTGGCGAGTCAGCTGGAGTCCACTGCTGCTGCG 423
DDIMM   460 CGGCTCGCTGAGGTCCGCGCTGCGGAGCTGGCAGCGCGGCTAAAGAGCACTGCTGCTGTT 519

LCIMM   661 AAGTCGTCGGCGGAGCAGGACCGCGAGAACACGAGGGCCGCGTTGGAGCAGCAGCTTCGT 720
KEIMM   424 AAGTCGTCGGCGGAGCAGGACCGCGAGAACACGAGGGCCACG------------------ 465
DDIMM   520 AAGTCCGCGATGGAGCAGGACCGCGAGAACACGAGGGCCACG------------------ 561
```

Figure 5

```
LCIMM   1   LEQQLRESEERAAELASQLEATAAAKSSAEQDRENTRATLEQQLRESEARAAELASQLEA   60
KEIMM   1   -EQQLRDSEERAAELMRKLEATAAAKSSAEQDRENTRATLEQQLRESEEHAAELKAQLES   59
DDIMM   1   -EQQLRESEARAAELKAELEATAAAKTSVEQEREKTRTALEG-------RAAELARKLEA   52


LCIMM   61  TAAAKMSAEQDRENTRATLEQQLRDSEERAAELASQLESTTAAKMSAEQDRESTRATLEQ   120
KEIMM   60  TAAAKTSAEQDRENTRAALEQRLRESEERAAELASQLEATAAAKSSAEQDRENTRATLEQ   119
DDIMM   53  TASAKNLVEQDRERTRATLEERLRIAEVRAAELAGVLEATAAAKTAVEQERERTRAALEQ   112


LCIMM   121 QLRDSEERAAELASQLESTTAAKMSAEQDRESTRATLEQQLRESEERAAELASQLESTTA   180
KEIMM   120 QLRESEARAAELASQLESTAAAKSSAEQDRENTRAT------------------------   155
DDIMM   113 QLRESEARAAELAAQLEAAAAAKTSVEQERENTRATLEERLRLAEVRAAELAARLKSTAA   172


LCIMM   181 AKMSAEQDRESTRATLEQQLRDSEERAAELASQLEATAAAKSSAEQDRENTRAALEQQLR   240
KEIMM   155 ------------------------------------------------------------   155
DDIMM   173 VKSAMEQDRENTRAT---------------------------------------------   187
```

Figure 6

```
LCIMM   1   LEQQLRESEERAAELASQLEATAAAKSSAEQDRENTRATLEQQLRESEARAAELASQLEA   60
DDIMM   1   ----------------------------------------EQQLRESEARAAELKAELEA   20


LCIMM   61  TAAAKMSAEQDRENTRATLEQQLRDSEERAAELASQLESTTAAKMSAEQDRESTRATLEQ   120
DDIMM   21  TAAAKTSVEQEREKTRTALEG-------RAAELARKLEATASAKNLVEQDRERTRATLEE   73


LCIMM   121 QLRDSEERAAELASQLESTTAAKMSAEQDRESTRATLEQQLRESEERAAELASQLESTTA   180
DDIMM   74  RLRIAEVRAAELAGVLEATAAAKTAVEQERERTRAALEQQLRESEARAAELAAQLEAAAA   133


LCIMM   181 AKMSAEQDRESTRATLEQQLRDSEERAAELASQLEATAAAKSSAEQDRENTRAALEQQLR   240
DDIMM   134 AKTSVEQERENTRATLEERLRLAEVRAAELAARLKSTAAVKSAMEQDRENTRAT------   187
```

App No.: NEW   Docket No.: 4661-0113PUS1
Inventor: Sarman SINGH et al.
Title: POLYPEPTIDES FOR THE DIAGNOSIS AND THERAPY
   OF LEISHAMANIASIS
NEW SHEET   Sheet 7 of 11

Figure 7

```
KEIMM    1  EQQLRDSEERAAELMRKLEATAAAKSSAEQ------------------------------ 30
DDIMM    1  EQQLRESEARAAELKAELEATAAAKTSVEQEREKTRTALEGRAAELARKLEATASAKNLV 60

KEIMM   30  --DRENTRATLEQQLRESEEHAAELKAQLESTAAAKTSAEQDRENTRAALEQRLRESEER 88
DDIMM   61  EQDRERTRATLRERLRIAEVRAAELAGVLEATAAAKTAVEQRERTRAALEQQLRESEAR 120

KEIMM   89  AAELASQLEATAAAKSSAEQDRENTRATLEQQLRESEARAAELASQLESTAAAKSSAEQD 148
DDIMM  121  AAELAAQLEAAAAAKTSVEQBRENTRATLEERLRLAEVRAAELAARLKSTAAVKSAMEQD 180

KEIMM  149  RENTRAT 155
DDIMM  181  RENTRAT 187
```

Figure 8

```
1             10           20           30           39
|             |            |            |            |

K E Q Q L R D S E T R A A E L K A E L E A T A A A K T S V E Q E R E K T R T A
L   G R A A E L A R K L E A T A S A K N L V E Q D R E R T R A T L   E R L R I
A   V         G V   K S A     V   T S M     E     N       A   Q Q       E
S   A         A Q                 S                                     L
```

Figure 9

```
1             10           20           30           39
|             |            |            |            |

L E Q Q L R D S E E R A A E L M R K L E A T A A A K S S A E Q D R E N T R A T
      R       E     A H         K A Q     S           T                   A
                                    A S
```

Figure 10

a)

b)

Figure 11

a)

b)

Figure 12

a)

b)

Figure 13

a)

b)

App No.: NEW
Inventor: Sarman SINGH et al.
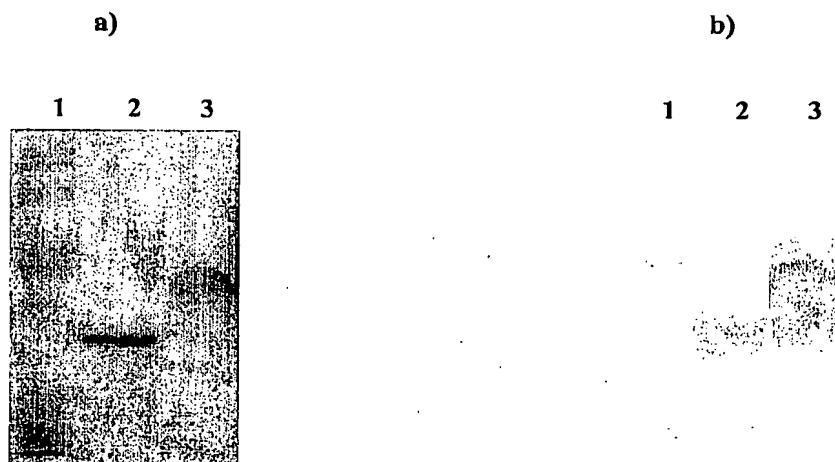Title: POLYPEPTIDES FOR THE DIAGNOSIS AND THERAPY
   OF LEISHAMANIASIS
NEW SHEET

Docket No.: 4661-0113PUS1

Sheet 10 of 11

BEST AVAILABLE COPY

Figure 14

a)

b)

Figure 15

Mean	0.1670	0.8665	0.1634	0.1396	0.1663	0.1636	0.1080
Std.Dev	0.0882	0.2182	0.0598	0.0584	0.0534	0.0615	0.0295

Figure 16

Mean	0.1290	0.9730	0.1300	0.1545	0.1456	0.1363	0.1219
Std.Dev	0.0716	0.2096	0.0419	0.0548	0.0705	0.0456	0.0796